



## SEQUENCE LISTING

<110> ENDO, NOBORU  
YOSHIDA, KOUKI  
AKIYOSHI, MIHO  
YOSHIDA, YASUKO  
OHSUMI, CHIEKO  
IGARASHI, DAISUKE

<120> GENE CAPABLE OF IMPARTING SALT STRESS RESISTANCE

<130> 279689US0XPCT

<140> 10/553,124

<141> 2005-10-14

<150> PCT/JP04/05403

<151> 2004-04-15

<150> JP 2003-113194

<151> 2003-04-17

<150> JP 2004-075932

<151> 2004-03-17

<160> 20

<170> PatentIn version 3.3

<210> 1

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<212> DNA

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<220>

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<222> (131) .. (1222)

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gacggcgcag atg gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg 169

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala

1

5

10

ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc 217

Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile

15

20

25

ggc acg cac acg gcg ctg cgc ctg ctg gag cag ggc tac ggc gtc acc	265
Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr	
30 35 40 45	
gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc	313
Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val	
50 55 60	
cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cgg	361
Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg	
65 70 75	
ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg	409
Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg	
80 85 90	
agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag	457
Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu	
95 100 105	
agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc	505
Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr	
110 115 120 125	
atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg	553
Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val	
130 135 140	
ttc tcg tcg tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc	601
Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys	
145 150 155	
gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag	649
Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys	
160 165 170	
ctc atc ctg gag gag ttg gcg cgg gac tac cag cgc gcg gac ccg ggc	697
Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly	
175 180 185	
tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc	745
Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser	
190 195 200 205	
tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg	793
Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu	
210 215 220	
ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc	841
Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val	

225	230	235	
tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac			889
Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr			
240	245	250	
ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag			937
Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys			
255	260	265	
ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca			985
Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr			
270	275	280	285
ggg cgc ggc aca tcc gtt ctc gag atg gtg gcg gcg ttc aag aag gca			1033
Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala			
290	295	300	
tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac			1081
Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp			
305	310	315	
gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctc gga			1129
Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly			
320	325	330	
tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac			1177
Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn			
335	340	345	
tgg gcc aag aag aac ccc tat ggc tac tgc ggc act gcc gaa aaa			1222
Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys			
350	355	360	
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tagccttcag gcccggcgct gttagccatt gcttgctatc gaggtagggtg gggttggaac			1462
tttgggcgcc cttgaacttc cattatcatc attcgcacag acggcacagt tgcgcagtga			1522
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 <213> Seashore Paspalum

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Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp  
35 40 45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile  
50 55 60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu  
65 70 75 80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp  
85 90 95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala  
100 105 110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu  
115 120 125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser  
130 135 140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp  
145 150 155 160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu  
165 170 175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile  
180 185 190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu  
 195 200 205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile  
 210 215 220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His  
 225 230 235 240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val  
 245 250 255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp  
 260 265 270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly  
 275 280 285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys  
 290 295 300

Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu  
 305 310 315 320

Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala  
 325 330 335

Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys  
 340 345 350

Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys  
 355 360

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 ttgacaccag accaactggg aatg 24

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 atctccatct cccaccccca tcgatccatt tgtgttggt ttaattccct gcgtgcatgc 180  
 gtgttggtga ataaggggcc ggttccatct gtacgtacgt gtactccgag acctatcgtc 240  
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 tgtgtgtgtg caactctgtt ctgatttgct atatataag 339

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 <212> DNA  
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 ctcagaccta tcggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180

agtttcgtac catctctctt gtcataacct catgtagatg gtcattttat tggaattagc	240
cttagccttc aggcccggcg ctgttaaaat ttgttttaca catggatttt ctcgctacgt	300
gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca	360
cgacggtggc tacgccctgt gttgtagtac tgtgaatatg atgtggtaat aacaataact	420
tgcagtgaga cttcagcttt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	480
aaaaaaaaaa aaaaaaa	497

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ctgccgaaaa atagagcgcg tgcattaatc agatctcttg actgaatttg tccatggttg	120
atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct	180
agctacgaag ttctgtacca tctctcttgt cataacctca tgtagatggc cattttattg	240
gaattagcct tagccttcag gcccggcgct gttaaaattt gttttacaca tggattttct	300
cgctacgtgt gatacatatt gtgtctgtaa taatcctgat cggagtttcc agtaataaaa	360
ccgatccacg acggtggcta cgccctgtgt tgtagt	396

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agccttcctt tccccgatcg ccgatccgat ccacaagcaa gcagccagg atg gtt tct	118

Met Val Ser

1

gcg	gtg	ctt	cgt	acc	atc	ctt	gtg	acg	ggc	ggc	gcc	ggc	tac	atc	ggc	166
Ala	Val	Leu	Arg	Thr	Ile	Leu	Val	Thr	Gly	Gly	Ala	Gly	Tyr	Ile	Gly	
5						10					15					
agc	cac	acc	gtg	ctg	ctg	ctg	ctg	cag	cag	gga	ttc	cgc	gtc	gtc	gtc	214
Ser	His	Thr	Val	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Phe	Arg	Val	Val	Val	
20					25					30					35	
gtc	gac	aac	ctc	gac	aac	gcc	tcc	gac	gtc	gcg	ctc	gcc	cgc	gtc	gcg	262
Val	Asp	Asn	Leu	Asp	Asn	Ala	Ser	Asp	Val	Ala	Leu	Ala	Arg	Val	Ala	
				40					45					50		
cag	ctc	gca	gca	agc	agc	aac	ggc	ggc	gcc	gcc	aac	ctc	gtc	ttc	cac	310
Gln	Leu	Ala	Ala	Ser	Ser	Asn	Gly	Gly	Ala	Ala	Asn	Leu	Val	Phe	His	
			55					60					65			
aag	gtt	gac	ctt	cgc	gac	agg	cac	gcg	ctg	gag	gac	atc	ttc	tcc	tcc	358
Lys	Val	Asp	Leu	Arg	Asp	Arg	His	Ala	Leu	Glu	Asp	Ile	Phe	Ser	Ser	
		70					75					80				
cac	agg	ttt	gag	gct	gtg	att	cat	ttt	gct	ggg	ctc	aaa	gct	gtt	ggc	406
His	Arg	Phe	Glu	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Gly	
	85					90					95					
gag	agc	gtg	cag	aag	ccg	ctg	ctt	tac	tac	gac	aac	aac	ctc	atc	ggc	454
Glu	Ser	Val	Gln	Lys	Pro	Leu	Leu	Tyr	Tyr	Asp	Asn	Asn	Leu	Ile	Gly	
100					105					110					115	
acc	atc	acc	ctc	ctc	gag	gtc	atg	gcc	gca	cat	ggc	tgc	aag	aag	ctg	502
Thr	Ile	Thr	Leu	Leu	Glu	Val	Met	Ala	Ala	His	Gly	Cys	Lys	Lys	Leu	
				120					125					130		
gtg	ttc	tcg	tca	tct	gca	act	gtc	tat	ggg	tgg	ccc	aag	gaa	gtg	cca	550
Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro	Lys	Glu	Val	Pro	
			135					140					145			
tgc	acc	gaa	gaa	ttc	cct	ctt	tgc	gcc	acc	aac	ccc	tat	ggg	cga	acc	598
Cys	Thr	Glu	Glu	Phe	Pro	Leu	Cys	Ala	Thr	Asn	Pro	Tyr	Gly	Arg	Thr	
		150					155					160				
aag	ctt	gtg	att	gaa	gat	atc	tgc	cgc	gac	gtc	cac	cgt	tca	gac	cct	646
Lys	Leu	Val	Ile	Glu	Asp	Ile	Cys	Arg	Asp	Val	His	Arg	Ser	Asp	Pro	
	165					170					175					
gat	tgg	aag	atc	ata	ctg	ctc	agg	tac	ttc	aac	cct	gtt	ggg	gct	cat	694
Asp	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His	
180					185					190					195	



cca agc gga cac atc ggt gaa gac ccc tct gga atc cca aac aac ctg	742
Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu	
200 205 210	
atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg cct cac ctc act	790
Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr	
215 220 225	
gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat	838
Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp	
230 235 240	
tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg	886
Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly	
245 250 255	
aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg	934
Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu	
260 265 275	
ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag	982
Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu	
280 285 290	
aag gtt tct ggc aag aaa atc cct ctg gtg ctt gct ggg cga aga cct	1030
Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro	
295 300 305	
gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag	1078
Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu	
310 315 320	
ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag	1126
Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln	
325 330 335	
tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac	1174
Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp	
340 345 350 355	
aac agc agc tgactgaaag caaatgcatg ctatgcatga tagggagatc	1223
Asn Ser Ser	
gagcagcaga ccacttacca ctgctagtaa aagaagtcga gtctcagaat accaccgtac	1283
gatatgcttac taaatagtcc gaggacggac ggacggatga tccatgtgtg gggcctcgta	1343
ttctcatttg tatagaggga cggagtagga gatccccagt cccatccatc cggttattg	1403
ttgctaccgt caatccatgt ttaagaaata aaccctatg catgtatgct tatcgatcta	1463

ctgtactagc taattatata ggcataatgta tatttggttag attccttatac aaaaaaaaaa 1523

aaaaaaaaaa aaaaaaa 1540

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<211> 358

<212> PRT

<213> Seashore Paspalum

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Met Val Ser Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly  
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Tyr Ile Gly Ser His Thr Val Leu Leu Leu Gln Gln Gly Phe Arg  
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Val Val Val Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala  
35 40 45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu  
50 55 60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile  
65 70 75 80

Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys  
85 90 95

Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn  
100 105 110

Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys  
115 120 125

Lys Lys Leu Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys  
130 135 140

Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr  
145 150 155 160

Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg  
165 170 175

Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val  
180 185 190

Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro  
195 200 205

Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro  
210 215 220

His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly  
225 230 235 240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala  
245 250 255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val  
260 265 270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala  
275 280 285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly  
290 295 300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala  
305 310 315 320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys  
325 330 335

Arg Asp Gln Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly  
340 345 350

Ser Pro Asp Asn Ser Ser

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<212> DNA  
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<400> 15  
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<220>  
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<213> Arabidopsis thaliana

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Val Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Ile Glu Ala Val Asp  
35 40 45

Arg Val Arg Glu Leu Val Gly Pro Asp Leu Ser Lys Lys Leu Asp Phe  
50 55 60

Asn Leu Gly Asp Leu Arg Asn Lys Gly Asp Ile Glu Lys Leu Phe Ser  
65 70 75 80

Lys Gln Arg Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val  
85 90 95

Gly Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val  
100 105 110

Gly Thr Ile Asn Leu Tyr Glu Thr Met Ala Lys Tyr Asn Cys Lys Met  
115 120 125

Met Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile  
130 135 140

Pro Cys Met Glu Asp Phe Glu Leu Lys Ala Met Asn Pro Tyr Gly Arg  
145 150 155 160

Thr Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu  
165 170 175

Pro Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala  
180 185 190

His Glu Ser Gly Ser Ile Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn  
 195 200 205

Leu Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu  
 210 215 220

Asn Val Tyr Gly His Asp Tyr Pro Thr Glu Asp Gly Ser Ala Val Arg  
 225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu  
 245 250 255

Arg Lys Leu Phe Ala Asp Pro Lys Ile Gly Cys Thr Ala Tyr Asn Leu  
 260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu  
 275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ser  
 290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Glu Lys Ala Glu Lys Glu  
 305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln  
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Trp Lys Trp Ala Asn Asn Asn Pro Trp Gly Tyr Gln Asn Lys Leu  
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<210> 19  
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Met Gly Ser Ser Val Glu Gln Asn Ile Leu Val Thr Gly Gly Ala Gly  
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Val	Thr	Ile	Ile	Asp	Asn	Leu	Asp	Asn	Ser	Val	Val	Glu	Ala	Val	His	35	40	45
Arg	Val	Arg	Glu	Leu	Val	Gly	Pro	Asp	Leu	Ser	Thr	Lys	Leu	Glu	Phe	50	55	60
Asn	Leu	Gly	Asp	Leu	Arg	Asn	Lys	Gly	Asp	Ile	Glu	Lys	Leu	Phe	Ser	65	70	75
Asn	Gln	Arg	Phe	Asp	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	85	90	95
Gly	Glu	Ser	Val	Gly	Asn	Pro	Arg	Arg	Tyr	Phe	Asp	Asn	Asn	Leu	Val	100	105	110
Gly	Thr	Ile	Asn	Leu	Tyr	Glu	Thr	Met	Ala	Lys	Tyr	Asn	Cys	Lys	Met	115	120	125
Met	Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Gln	Pro	Glu	Ile	Val	130	135	140
Pro	Cys	Val	Glu	Asp	Phe	Glu	Leu	Gln	Ala	Met	Asn	Pro	Tyr	Gly	Arg	145	150	155
Thr	Lys	Leu	Phe	Leu	Glu	Glu	Ile	Ala	Arg	Asp	Ile	His	Ala	Ala	Glu	165	170	175
Pro	Glu	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	180	185	190
His	Glu	Ser	Gly	Arg	Ile	Gly	Glu	Asp	Pro	Lys	Gly	Ile	Pro	Asn	Asn	195	200	205
Leu	Met	Pro	Tyr	Ile	Gln	Gln	Val	Ala	Val	Gly	Arg	Leu	Pro	Glu	Leu	210	215	220



Asn Val Phe Gly His Asp Tyr Pro Thr Met Asp Gly Ser Ala Val Arg  
 225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Val Ala Ala Leu  
 245 250 255

Asn Lys Leu Phe Ser Asp Ser Lys Ile Gly Cys Thr Ala Tyr Asn Leu  
 260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ser Ser Phe Glu  
 275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ala  
 290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Gln Lys Ala Glu Lys Glu  
 305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln  
 325 330 335

Trp Asn Trp Ala Asn Lys Asn Pro Trp Gly Phe Gln Lys Lys Pro  
 340 345 350

<210> 20

<211> 354

<212> PRT

<213> Cyamopsis tetragonoloba

<400> 20

Met Val Ser Ser Arg Met Ala Ser Gly Glu Thr Ile Leu Val Thr Gly  
 1 5 10 15

Gly Ala Gly Phe Ile Gly Ser His Thr Val Val Gln Leu Leu Lys Gln  
 20 25 30

Gly Phe His Val Ser Ile Ile Asp Asn Leu Tyr Asn Ser Val Ile Asp  
 35 40 45

Ala Val His Arg Val Arg Leu Leu Val Gly Pro Leu Leu Ser Ser Asn  
50 55 60

Leu His Phe His His Gly Asp Leu Arg Asn Ile His Asp Leu Asp Ile  
65 70 75 80

Leu Phe Ser Lys Thr Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu  
85 90 95

Lys Gly Val Gly Glu Ser Val Leu Asn Pro Ser Asn Tyr Tyr Asp Asn  
100 105 110

Asn Leu Val Ala Thr Ile Asn Leu Phe Gln Val Met Ser Lys Phe Asn  
115 120 125

Cys Lys Lys Leu Val Ile Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro  
130 135 140

Asp Gln Ile Pro Cys Val Glu Asp Ser Asn Leu His Ala Met Asn Pro  
145 150 155 160

Tyr Gly Arg Ser Lys Leu Phe Val Glu Glu Val Ala Arg Asp Ile Gln  
165 170 175

Arg Ala Glu Ala Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro  
180 185 190

Val Gly Ala His Glu Ser Gly Gln Ile Gly Glu Asp Pro Arg Gly Leu  
195 200 205

Pro Asn Asn Leu Met Pro Tyr Ile Gln Gln Val Ala Val Ala Arg Leu  
210 215 220

Pro Glu Leu Asn Ile Tyr Gly His Asp Tyr Pro Thr Lys Asp Gly Thr  
225 230 235 240

Ala Ile Arg Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile

245

250

255

Ala Ala Leu Arg Lys Leu Phe Thr Thr Asp Asn Ile Gly Cys Thr Ala  
 260 265 270

Tyr Asn Leu Gly Thr Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala  
 275 280 285

Ala Phe Glu Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Met Cys Pro  
 290 295 300

Arg Arg Pro Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Glu Lys Ala  
 305 310 315 320

Glu Lys Glu Leu Gly Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys  
 325 330 335

Arg Asp Gln Trp Lys Trp Ala Ser Asn Asn Pro Trp Gly Tyr Gln Gly  
 340 345 350

Lys His